



SEQUENCE LISTING

<110> HOSTETTER, Margaret K.
DEVORE-CARTER, Denise

<120> ANTIBODIES TO THE PROPEPTIDE OF CANDIDA ALBICANS

<130> P07274US02/BAS

<140> US 09/964,858

<141> 2001-09-28

<150> US 60/237,082

<151> 2000-09-28

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 1664

<212> PRT

<213> Candida albicans

<400> 1

Met Asn Ser Thr Pro Ser Lys Leu Leu Pro Ile Asp Lys His Ser His
1 5 10 15

Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro
20 25 30

Thr Lys Pro Leu Asn Phe Pro Arg Thr Asn Ser Lys Pro Ser Leu Asp
35 40 45

Pro Asn Ser Ser Ser Asp Thr Tyr Thr Ser Glu Gln Asp Gln Glu Lys
50 55 60

Gly Lys Glu Glu Lys Lys Asp Thr Ala Phe Gln Thr Ser Phe Asp Arg
65 70 75 80

Asn Phe Asp Leu Asp Asn Ser Ile Asp Ile Gln Gln Thr Ile Gln His
85 90 95

Gln Gln Gln Gln Pro Gln Gln Gln Gln Leu Ser Gln Thr Asp Asn
100 105 110

Asn Leu Ile Asp Glu Phe Ser Phe Gln Thr Pro Met Thr Ser Thr Leu
115 120 125

Asp Leu Thr Lys Gln Asn Pro Thr Val Asp Lys Val Asn Glu Asn His
130 135 140

Ala Pro Thr Tyr Ile Asn Thr Ser Pro Asn Lys Ser Ile Met Lys Lys
145 150 155 160

Ala Thr Pro Lys Ala Ser Pro Lys Lys Val Ala Phe Thr Val Thr Asn
165 170 175

Pro Glu Ile His His Tyr Pro Asp Asn Arg Val Glu Glu Glu Asp Gln
180 185 190

Ser Gln Gln Lys Glu Asp Ser Val Glu Pro Pro Leu Ile Gln His Gln
195 200 205

Trp Lys Asp Pro Ser Gln Phe Asn Tyr Ser Asp Glu Asp Thr Asn Ala
210 215 220

Ser Val Pro Pro Thr Pro Pro Leu His Thr Thr Lys Pro Thr Phe Ala
225 230 235 240

Gln Leu Leu Asn Lys Asn Asn Glu Val Asn Ser Glu Pro Glu Ala Leu
245 250 255

Thr Asp Met Lys Leu Lys Arg Glu Asn Phe Ser Asn Leu Ser Leu Asp
260 265 270

Glu Lys Val Asn Leu Tyr Leu Ser Pro Thr Asn Asn Asn Asn Ser Lys
275 280 285

Asn Val Ser Asp Met Asp Ser His Leu Gln Asn Leu Gln Asp Ala Ser
290 295 300

Lys Asn Lys Thr Asn Glu Asn Ile His Asn Leu Ser Phe Ala Leu Lys
305 310 315 320

Ala Pro Lys Asn Asp Ile Glu Asn Pro Leu Asn Ser Leu Thr Asn Ala
325 330 335

Asp Ile Ser Leu Arg Ser Ser Gly Ser Ser Gln Ser Ser Leu Gln Ser
340 345 350

Leu Arg Asn Asp Asn Arg Val Leu Glu Ser Val Pro Gly Ser Pro Lys
355 360 365

Lys Val Asn Pro Gly Leu Ser Leu Asn Asp Gly Ile Lys Gly Phe Ser
370 375 380

Asp Glu Val Val Glu Ser Leu Leu Pro Arg Asp Leu Ser Arg Asp Lys
385 390 395 400

Leu Glu Thr Thr Lys Glu His Asp Ala Pro Glu His Asn Asn Glu Asn
405 410 415

Phe Ile Asp Ala Lys Ser Thr Asn Thr Asn Lys Gly Gln Leu Leu Val
420 425 430

Ser Ser Asp Asp His Leu Asp Ser Phe Asp Arg Ser Tyr Asn His Thr
435 440 445

Glu Gln Ser Ile Leu Asn Leu Leu Asn Ser Ala Ser Gln Ser Gln Ile
450 455 460

Ser Leu Asn Ala Leu Glu Lys Gln Arg Gln Thr Gln Glu Gln Glu Gln
465 470 475 480

Thr Gln Ala Ala Glu Pro Glu Glu Glu Thr Ser Phe Ser Asp Asn Ile
485 490 495

Lys Val Lys Gln Glu Pro Lys Ser Asn Leu Glu Phe Val Lys Val Thr
500 505 510

Ile Lys Lys Glu Pro Val Ser Ala Thr Glu Ile Lys Ala Pro Lys Arg
515 520 525

Glu Phe Ser Ser Arg Ile Leu Arg Ile Lys Asn Glu Asp Glu Ile Ala
530 535 540

Glu Pro Ala Asp Ile His Pro Lys Lys Glu Asn Glu Ala Asn Ser His
545 550 555 560

Val Glu Asp Thr Asp Ala Leu Leu Lys Lys Ala Leu Asn Asp Asp Glu
565 570 575

Glu Ser Asp Thr Thr Gln Asn Ser Thr Lys Met Ser Ile Arg Phe His

580	585	590
Ile Asp Ser Asp Trp Lys Leu Glu Asp Ser Asn Asp Gly Asp Arg Glu		
595	600	605
Asp Asn Asp Asp Ile Ser Arg Phe Glu Lys Ser Asp Ile Leu Asn Asp		
610	615	620
Val Ser Gln Thr Ser Asp Ile Ile Gly Asp Lys Tyr Gly Asn Ser Ser		
625	630	635
Ser Glu Ile Thr Thr Lys Thr Leu Ala Pro Pro Arg Ser Asp Asn Asn		
645	650	655
Asp Lys Glu Asn Ser Lys Ser Leu Glu Asp Pro Ala Asn Asn Glu Ser		
660	665	670
Leu Gln Gln Gln Leu Glu Val Pro His Thr Lys Glu Asp Asp Ser Ile		
675	680	685
Leu Ala Asn Ser Ser Asn Ile Ala Pro Pro Glu Glu Leu Thr Leu Pro		
690	695	700
Val Val Glu Ala Asn Asp Tyr Ser Ser Phe Asn Asp Val Thr Lys Thr		
705	710	715
Phe Asp Ala Tyr Ser Ser Phe Glu Glu Ser Leu Ser Arg Glu His Glu		
725	730	735
Thr Asp Ser Lys Pro Ile Asn Phe Ile Ser Ile Trp His Lys Gln Glu		
740	745	750
Lys Gln Lys Lys His Gln Ile His Lys Val Pro Thr Lys Gln Ile Ile		
755	760	765
Ala Ser Tyr Gln Gln Tyr Lys Asn Glu Gln Glu Ser Arg Val Thr Ser		
770	775	780
Asp Lys Val Lys Ile Pro Asn Ala Ile Gln Phe Lys Lys Phe Lys Glu		
785	790	795
Val Asn Val Met Ser Arg Arg Val Val Ser Pro Asp Met Asp Asp Leu		
805	810	815

Asn Val Ser Gln Phe Leu Pro Glu Leu Ser Glu Asp Ser Gly Phe Lys
820 825 830

Asp Leu Asn Phe Ala Asn Tyr Ser Asn Asn Thr Asn Arg Pro Arg Ser
835 840 845

Phe Thr Pro Leu Ser Thr Lys Asn Val Leu Ser Asn Ile Asp Asn Asp
850 855 860

Pro Asn Val Val Glu Pro Pro Glu Pro Lys Ser Tyr Ala Glu Ile Arg
865 870 875 880

Asn Ala Arg Arg Leu Ser Ala Asn Lys Ala Ala Pro Asn Gln Ala Pro
885 890 895

Pro Leu Pro Pro Gln Arg Gln Pro Ser Ser Thr Arg Ser Asn Ser Asn
900 905 910

Lys Arg Val Ser Arg Phe Arg Val Pro Thr Phe Glu Ile Arg Arg Thr
915 920 925

Ser Ser Ala Leu Ala Pro Cys Asp Met Tyr Asn Asp Ile Phe Asp Asp
930 935 940

Phe Gly Ala Gly Ser Lys Pro Thr Ile Lys Ala Glu Gly Met Lys Thr
945 950 955 960

Leu Pro Ser Met Asp Lys Asp Asp Val Lys Arg Ile Leu Asn Ala Lys
965 970 975

Lys Gly Val Thr Gln Asp Glu Tyr Ile Asn Ala Lys Leu Val Asp Gln
980 985 990

Lys Pro Lys Lys Asn Ser Ile Val Thr Asp Pro Glu Asp Arg Tyr Glu
995 1000 1005

Glu Leu Gln Gln Thr Ala Ser Ile His Asn Ala Thr Ile Asp Ser
1010 1015 1020

Ser Ile Tyr Gly Arg Pro Asp Ser Ile Ser Thr Asp Met Leu Pro
1025 1030 1035

Tyr	Leu	Ser	Asp	Glu	Leu	Lys	Lys	Pro	Pro	Thr	Ala	Leu	Leu	Ser
1040						1045					1050			
Ala	Asp	Arg	Leu	Phe	Met	Glu	Gln	Glu	Val	His	Pro	Leu	Arg	Ser
1055						1060					1065			
Asn	Ser	Val	Leu	Val	His	Pro	Gly	Ala	Gly	Ala	Ala	Thr	Asn	Ser
1070						1075					1080			
Ser	Met	Leu	Pro	Glu	Pro	Asp	Phe	Glu	Leu	Ile	Asn	Ser	Pro	Ala
1085						1090					1095			
Arg	Asn	Val	Ser	Asn	Asn	Ser	Asp	Asn	Val	Ala	Ile	Ser	Gly	Asn
1100						1105					1110			
Ala	Ser	Thr	Ile	Ser	Phe	Asn	Gln	Leu	Asp	Met	Asn	Phe	Asp	Asp
1115						1120					1125			
Gln	Ala	Thr	Ile	Gly	Gln	Lys	Ile	Gln	Glu	Gln	Pro	Ala	Ser	Lys
1130						1135					1140			
Ser	Ala	Asn	Thr	Val	Arg	Gly	Asp	Asp	Asp	Gly	Leu	Ala	Ser	Ala
1145						1150					1155			
Pro	Glu	Thr	Pro	Arg	Thr	Pro	Thr	Lys	Lys	Glu	Ser	Ile	Ser	Ser
1160						1165					1170			
Lys	Pro	Ala	Lys	Leu	Ser	Ser	Ala	Ser	Pro	Arg	Lys	Ser	Pro	Ile
1175						1180					1185			
Lys	Ile	Gly	Ser	Pro	Val	Arg	Val	Ile	Lys	Lys	Asn	Gly	Ser	Ile
1190						1195					1200			
Ala	Gly	Ile	Glu	Pro	Ile	Pro	Lys	Ala	Thr	His	Lys	Pro	Lys	Lys
1205						1210					1215			
Ser	Phe	Gln	Gly	Asn	Glu	Ile	Ser	Asn	His	Lys	Val	Arg	Asp	Gly
1220						1225					1230			
Gly	Ile	Ser	Pro	Ser	Ser	Gly	Ser	Glu	His	Gln	Gln	His	Asn	Pro
1235						1240					1245			

Ser Met Val Ser Val Pro Ser Gln Tyr Thr Asp Ala Thr Ser Thr
1250 1255 1260

Val Pro Asp Glu Asn Lys Asp Val Gln His Lys Pro Arg Glu Lys
1265 1270 1275

Gln Lys Gln Lys His His His Arg His His His His His His Lys
1280 1285 1290

Gln Lys Thr Asp Ile Pro Gly Val Val Asp Asp Glu Ile Pro Asp
1295 1300 1305

Val Gly Leu Gln Glu Arg Gly Lys Leu Phe Phe Arg Val Leu Gly
1310 1315 1320

Ile Lys Asn Ile Asn Leu Pro Asp Ile Asn Thr His Lys Gly Arg
1325 1330 1335

Phe Thr Leu Thr Leu Asp Asn Gly Val His Cys Val Thr Thr Pro
1340 1345 1350

Glu Tyr Asn Met Asp Asp His Asn Val Ala Ile Gly Lys Glu Phe
1355 1360 1365

Glu Leu Thr Val Ala Asp Ser Leu Glu Phe Ile Leu Thr Leu Lys
1370 1375 1380

Ala Ser Tyr Glu Lys Pro Arg Gly Thr Leu Val Glu Val Thr Glu
1385 1390 1395

Lys Lys Val Val Lys Ser Arg Asn Arg Leu Ser Arg Leu Phe Gly
1400 1405 1410

Ser Lys Asp Ile Ile Thr Thr Thr Lys Phe Val Pro Thr Glu Val
1415 1420 1425

Lys Asp Thr Trp Ala Asn Lys Phe Ala Pro Asp Gly Ser Phe Ala
1430 1435 1440

Arg Cys Tyr Ile Asp Leu Gln Gln Phe Glu Asp Gln Ile Thr Gly
1445 1450 1455

Lys Ala Ser Gln Phe Asp Leu Asn Cys Phe Asn Glu Trp Glu Thr

1460		1465		1470
Met Ser Asn Gly Asn Gln Pro	Met Lys Arg Gly Lys	Pro Tyr Lys		
1475	1480	1485		
Ile Ala Gln Leu Glu Val Lys	Met Leu Tyr Val Pro	Arg Ser Asp		
1490	1495	1500		
Pro Arg Glu Ile Leu Pro Thr	Ser Ile Arg Ser Ala	Tyr Glu Ser		
1505	1510	1515		
Ile Asn Glu Leu Asn Asn Glu	Gln Asn Asn Tyr Phe	Glu Gly Tyr		
1520	1525	1530		
Leu His Gln Glu Gly Gly Asp	Cys Pro Ile Phe Lys	Lys Arg Phe		
1535	1540	1545		
Phe Lys Leu Met Gly Thr Ser	Leu Leu Ala His Ser	Glu Ile Ser		
1550	1555	1560		
His Lys Thr Arg Ala Lys Ile	Asn Leu Ser Lys Val	Val Asp Leu		
1565	1570	1575		
Ile Tyr Val Asp Lys Glu Asn	Ile Asp Arg Ser Asn	His Arg Asn		
1580	1585	1590		
Phe Ser Asp Val Leu Leu Leu	Asp His Ala Phe Lys	Ile Lys Phe		
1595	1600	1605		
Ala Asn Gly Glu Leu Ile Asp	Phe Cys Ala Pro Asn	Lys His Glu		
1610	1615	1620		
Met Lys Ile Trp Ile Gln Asn	Leu Gln Glu Ile Ile	Tyr Arg Asn		
1625	1630	1635		
Arg Phe Arg Arg Gln Pro Trp	Val Asn Leu Met Leu	Gln Gln Gln		
1640	1645	1650		
Gln Gln Gln Gln Gln Gln	Ser Ser Gln Gln			
1655	1660			

<210> 2
<211> 5194

<212> DNA

<213> *Candida albicans*

<400> 2

ccccaaaaag ataaaataaa aacaaaacaa aacaaaagta ctaacaaatt attgaaactt	60
ttaatttttta ataaagaatc agtagatcta ttgttaaaag aaatgaactc aactccaagt	120
aaattatttac cgatagataa acatttctcat ttacaattac agcctcaatc gtcctcggca	180
tcaatatttta attccccaac aaaaccattg aatttcccca gaacaaattc caagccgagt	240
ttagatccaa attcaagctc tgatacctac actagogaac aagatcaaga gaaagggaaa	300
gaagagaaaa aggacacagc ctttcaaaca tcttttgata gaaattttga tcttgataat	360
tcaatcgata tacaacaaac aattcaacat cagcaacaac agccacaaca acaacaacaa	420
ctctcacaaa cgcacaataa ttttaattgat gaattttctt ttcaaacacc gatgacttcg	480
acttttagacc taaccaagca aaatccaact gtggacaaaag tgaatgaaaa tcatgcacca	540
acttatataa atacctcccc caacaaatca ataatgaaaa aggcaactcc taaagcgtca	600
cctaaaaaag ttgcattttac tgtaactaat cccgaaattc atcattatcc agataataga	660
gtcgaggaag aagatcaaag tcaacaaaaa gaagattcag ttgagccacc cttaatataa	720
catcaatgga aagatccttc tcaattcaat tattctgatg aagatacaaa tgcttcagtt	780
ccaccaacac caccacttca tacgacgaaa cctacttttg cgcaattatt gaacaaaaac	840
aacgaagtca atctggaacc agaggcattg acagatatga aattaaagcg cgaaaatttc	900
agcaattttat cattagatga aaaagtcaat ttatatctta gtcccactaa taataacaat	960
agtaagaatg tgtcagatat ggatctgcat ttacaaaact tgcaagacgc ttcgaaaaac	1020
aaaactaatg aaaatattca caatttgtca tttgctttta aagcaccaaa gaatgatatt	1080
gaaaacccat taaactcatt gactaacgca gatattctgt taagatcatc tggatcatca	1140
caatcgtcat tacaatcttt gaggaatgac aatcgtgtct tggaatcagt gcctgggtca	1200
cctaagaagg ttaatcctgg attgtctttg aatgacggca taaaggggtt ctctgatgag	1260
gttggttgaat cattacttcc tcgtgactta tctcgagaca aattagagac tacaaaagaa	1320
catgatgcac cagaacacaa caatgagaat tttattgatg ctaaatcgac taataccaat	1380
aagggacaac tottagtata atctgatgat catttggaact cttttgatag atcctataac	1440
cacactgaac aatcaatttt gaatcttttg aatagtgcac cacaatctca aatttcgtta	1500
aatgcattgg aaaaacaaag gcaaacacag gaacaagaac aaacacaagc ggcagagcct	1560
gaagaagaaa cttcgttttag tgataatatc aaagttaaac aagagccaaa gagcaatttg	1620

gagtttgtca aggttaccat caagaaagaa ccagttcttg ccacggaaat aaaagctcca	1680
aaaagagaat tttcaagtcg aatattaaga ataaaaaatg aagatgaaat tgccgaacca	1740
gctgatattc atcctaaaaa agaaaatgaa gcaaacagtc atgtcgaaga tactgatgca	1800
ttgttgaaga aagcacttaa tgatgatgag gaatctgaca cgacccaaaa ctcaacgaaa	1860
atgtcaattc gttttcatat tgatagtgat tggaaattgg aagacagtaa tgatggcgat	1920
agagaagata atgatgatat ttctcgtttt gagaaatcag atattttgaa cgacgtatca	1980
cagacttctg atattattgg tgacaaatat ggaaactcat caagtgaaat aaccaccaa	2040
acattagcac cccaagatc ggacaacaat gacaaggaga attctaaatc tttggaagat	2100
ccagctaata atgaatcatt gcaacaacaa ttggagggtac cgcatacaaa agaagatgat	2160
agcatttttag ccaactcgtc caatattgct ccacctgaag aattgacttt gcccgtagtg	2220
gaagcaaagtg attattcatc ttttaatgac gtgaccaaaa cttttgatgc atactcaagc	2280
tttgaagagt cattatctag agagcacgaa actgattcaa aaccaattaa tttcatatca	2340
atttggcata aacaagaaaa gcagaagaaa catcaaattc ataaagttcc aactaaacag	2400
atcattgcta gttatcaaca atacaaaaac gaacaagaat ctctgtgttac tagtgataaa	2460
gtgaaaatcc caaatgccat acaattcaag aaattcaaag aggtaaatgt catgtcaaga	2520
agagttgtta gtccagacat ggatgatttg aatgtatctc aatttttacc agaattatct	2580
gaagactctg gatttaaaga tttgaatttt gccaaactact ccaataacac caacagacca	2640
agaagtttta ctccattgag cactaaaaat gtcttgtcga atattgataa cgatccta	2700
gttgttgaac ctctgaacc gaaatcatat gctgaaatta gaaatgctag acggttatca	2760
gctaataagg cagcgccaaa tcaggcacca ccattgccac cacaacgaca accatcttca	2820
actcgttcca attcaaataa acgagtgtcc agatttagag tgcccacatt tgaaattaga	2880
agaacttctt cagcattagc accttgtgac atgtataatg atatttttga tgatttcggt	2940
gcgggttcta aaccaactat aaaggcagaa ggaatgaaaa cattgccaag tatggataaa	3000
gatgatgtca agaggatttt gaatgcaaag aaagggtgtga ctcaagatga atatataaat	3060
gccaaacttg ttgatcaaaa acctaaaaag aattcaattg tcaccgatcc cgaagaccga	3120
tatgaagaat tacaacaaac tgctctata cacaatgcc ccatcgattc aagtatttat	3180
ggccgaccag actccatttc taccgacatg ttgccttctc ttagtgatga attgaaaaaa	3240
ccacctacgg ctttattatc tgctgatcgt ttgtttatgg aacaagaagt acatccgtta	3300

agatcaaact ctgttttgggt tcaccaggg gcaggagcag caactaatc ttcaatgtta	3360
ccagagccag attttgaatt aatcaattca cctgctagaa atgtgctgaa caacagtgat	3420
aatgtcgcca tcagtggtaa tgctagtact attagtttta accaattgga tatgaatttt	3480
gatgaccaag ctacaattgg tcaaaaaatc caagagcaac ctgcttcaaa atccgccaat	3540
actgttcgtg gtgatgatga tggattggcc agtgcacctg aaacaccaag aactcctacc	3600
aaaaaggagt ccatatcaag caagcctgcc aagctttctt ctgcctcccc tagaaaatca	3660
ccaattaaga ttggttcacc agttcgagtt attaagaaaa atggatcaat tgctggcatt	3720
gaaccaatcc caaaagccac tcacaaaccg aagaaatcat tccaaggaaa cgagatttca	3780
aaccataaag tacgagatgg tggaaatttca ccaagctccg gatcagagca tcaacagcat	3840
aatcctagta tggtttctgt tccttcacag tatactgatg ctacttcaac ggttccagat	3900
gaaaacaaag atgttcaaca caagcctcgt gaaaagcaaa agcaaaagca tcaccatcgc	3960
catcatcatc atcatcataa acaaaaaact gatattccgg gtgttggtga tgatgaaatt	4020
cctgatgtag gattacaaga acgaggcaaa ttattcttta gagttttagg aattaagaat	4080
atcaatttac cggatattaa tactcacaaa ggaagattca ctttaacggt ggataatgga	4140
gtgcattgtg ttactacacc agaatacaac atggacgacc ataatgttgc cataggtaaa	4200
gaatttgagt tgacagttgc tgattcatta gagtttattt taactttgaa ggcatcatat	4260
gaaaaacctc gtggtacatt agtagaagtg actgaaaaga aagttgtcaa atcaagaaat	4320
agattgagtc gattatttgg atcgaaagat attatcacca cgacaaagtt tgtgccact	4380
gaagtcaaag atacctgggc taataagttt gctcctgatg gttcatttgc tagatgttac	4440
attgatttac aacaatttga agaccaaac accggtaaag catcacagtt tgatctcaat	4500
tgttttaatg aatgggaaac tatgagtaat ggcaatcaac caatgaaaag aggcaaacct	4560
tataagattg ctcaattgga agttaaagt ttgtatgttc cacgatcaga tccaagagaa	4620
atattacca ccagcattag atccgcatat gaaagcatca atgaattaaa caatgaacag	4680
aataattact ttgaaggtta ttacatcaa gaaggaggtg attgtccaat ttttaagaaa	4740
cgttttttca aattaatggg cacttcttta ttggctcata gtgaaatata tcataaaact	4800
agagccaaaa ttaatttatc aaaagttggt gatttgattt atgttgataa agaaaacatt	4860
gatcgttcca atcatcgaaa tttcagtgat gtgttattgt tggatcatgc attcaaaatc	4920
aaatttgcta atggtgagtt gattgatttt tgtgctccta ataaacatga aatgaaaata	4980
tggattcaaa atttacaaga aattatctat agaaatcggg tcagacgtca accatgggta	5040

aatttgatgc ttcaacaaca acaacaacaa caacaacaac aaagctccca acagtaattg 5100
aaaggtctac ttttgatgtt ttttaatttta attggcaaata atatgcccat tttgtattat 5160
cttttagtgt aatagcgttt tttttttttc cagt 5194

<210> 3
<211> 4
<212> PRT
<213> Candida albicans

<400> 3

Asp His Asn Ser
1

<210> 4
<211> 7
<212> PRT
<213> Candida albicans

<400> 4

Asp His Asn Arg Gly Asp Ser
1 5

<210> 5
<211> 5
<212> PRT
<213> Candida albicans

<400> 5

Phe Val Gln Asn Leu
1 5

<210> 6
<211> 11
<212> PRT
<213> Candida albicans

<400> 6

Asn Asn Val Val Phe Thr Asn Lys Glu Leu Glu
1 5 10

<210> 7
<211> 11
<212> PRT
<213> Candida albicans

<400> 7

Phe Ala Gln Leu Leu Asn Lys Asn Asn Glu Val
1 5 10

<210> 8

<211> 5

<212> PRT

<213> Candida albicans

<400> 8

Asn Ser Glu Pro Glu
1 5

<210> 9

<211> 15

<212> PRT

<213> Candida albicans

<400> 9

Lys Ser Ile Met Lys Lys Ala Thr Pro Lys Ala Ser Pro Lys Lys
1 5 10 15

<210> 10

<211> 4

<212> PRT

<213> Candida albicans

<400> 10

Lys Leu Arg Arg
1

<210> 11

<211> 16

<212> PRT

<213> Candida albicans

<400> 11

Lys Ala Ala Ala Lys Lys Ala Pro Ala Lys Lys Ala Ala Ala Lys Lys
1 5 10 15

<210> 12

<211> 15

<212> PRT

<213> Candida albicans

<400> 12

Lys Ser Ile Met Lys Lys Ala Thr Pro Lys Ala Ser Pro Lys Lys
1 (5 10 15

<210> 13

<211> 6

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid

<400> 13

Asp Asp Xaa His Asn Ser
1 5